

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/715,909
DATE: 05/15/2001
TIME: 11:31:45

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05152001\I715909.raw

ENTERED

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4 <110> APPLICANT: Flannagan, Ronald D.
5   Mathis, John P.
6   Meyer, Terry E.
9 <120> TITLE OF INVENTION: Novel Bt Toxin Receptors From
10  Lepidopteran Insects and Methods of Use
13 <130> FILE REFERENCE: 35718/204664
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/715,909
C--> 15 <141> CURRENT FILING DATE: 2000-11-17
15 <150> PRIOR APPLICATION NUMBER: 60/166,285
16 <151> PRIOR FILING DATE: 1999-11-18
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 5498
24 <212> TYPE: DNA
25 <213> ORGANISM: Ostrinia nubilalis
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (162)...(5312)
31 <400> SEQUENCE: 1
32 cataataaca ataaagagga agtgtgtgtg aaaaacgaag aagttaataa acctggataa 60
33 ttaaaccctga aaaaaaccgg tgtttaagtg gaatttttgc tgaaggacaa ccgtgggata 120
34 gctcaaatat taaaattcta cataactaag gatcatgcaa a atg ggg gtt gag agg 176
35                                     Met Gly Val Glu Arg
36                                     1 5
38 ttc ttc cca gca gtg cta ctg gtc tct tta gcc tct gcc gca cta gcc 224
39 Phe Phe Pro Ala Val Leu Leu Val Ser Leu Ala Ser Ala Ala Leu Ala
40 10 15 20
42 aac caa cga tgt tcg tac att atc gca ata cca aga ccg gag act ccg 272
43 Asn Gln Arg Cys Ser Tyr Ile Ile Ala Ile Pro Arg Pro Glu Thr Pro
44 25 30 35
46 gaa ctg ccg cct att gat tac gaa gga aaa tca tgg agt gaa cag cct 320
47 Glu Leu Pro Pro Ile Asp Tyr Glu Gly Lys Ser Trp Ser Glu Gln Pro
48 40 45 50
50 cta ata ccc ggc ccg acc cga gag gaa gta tgt atg gag aac ttc tta 368
51 Leu Ile Pro Gly Pro Thr Arg Glu Glu Val Cys Met Glu Asn Phe Leu
52 55 60 65
54 ccg gat caa atg att cag gtc ata tac atg gag gaa gaa atc gaa gga 416
55 Pro Asp Gln Met Ile Gln Val Ile Tyr Met Glu Glu Glu Ile Glu Gly
56 70 75 80 85
58 gac gtc atc att gcg aag ctt aac tat caa ggg tcc aac acg ccg gtg 464
59 Asp Val Ile Ile Ala Lys Leu Asn Tyr Gln Gly Ser Asn Thr Pro Val
60 90 95 100
62 ctg tcg att atg tca ggc cag ccc aga gcc cag ctg ggc cct gag ttt 512
63 Leu Ser Ile Met Ser Gly Gln Pro Arg Ala Gln Leu Gly Pro Glu Phe
64 105 110 115
66 cga cag aat gaa gca gac ggc caa tgg agc ctt gtt att acg caa aga 560

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67 Arg Gln Asn Glu Ala Asp Gly Gln Trp Ser Leu Val Ile Thr Gln Arg
68      120      125      130
70 caa gac tac gag aca gca acc atg cag agc tat gtg ttc tca atc caa      608
71 Gln Asp Tyr Glu Thr Ala Thr Met Gln Ser Tyr Val Phe Ser Ile Gln
72      135      140      145
74 gtg gag ggt gaa tca cag gcc gta ctg gtg gcg ctg gag ata gtc aac      656
75 Val Glu Gly Glu Ser Gln Ala Val Leu Val Ala Leu Glu Ile Val Asn
76 150      155      160      165
78 atc gac gac aat ccg ccc atc ctg caa gtg gtc agc gcc tgc gta att      704
79 Ile Asp Asp Asn Pro Pro Ile Leu Gln Val Val Ser Ala Cys Val Ile
80      170      175      180
82 cca gaa cat ggc gag gct aga ctg acc gac tgc gtg tac caa gtg tca      752
83 Pro Glu His Gly Glu Ala Arg Leu Thr Asp Cys Val Tyr Gln Val Ser
84      185      190      195
86 gac cgc gac ggt gaa atc agc acc cgc ttc atg acg ttc cgt gtc gac      800
87 Asp Arg Asp Gly Glu Ile Ser Thr Arg Phe Met Thr Phe Arg Val Asp
88      200      205      210
90 agc agc agg gct gca gat gaa agc atc ttc tac atg gtt gga gaa tac      848
91 Ser Ser Arg Ala Ala Asp Glu Ser Ile Phe Tyr Met Val Gly Glu Tyr
92      215      220      225
94 gac ccc agc gac tgg ttc aat atg aag atg act gtg ggg atc aat tcg      896
95 Asp Pro Ser Asp Trp Phe Asn Met Lys Met Thr Val Gly Ile Asn Ser
96 230      235      240      245
98 ccc ttg aac ttc gag aca act cag ctt cat ata ttt agc gtc aca gct      944
99 Pro Leu Asn Phe Glu Thr Thr Gln Leu His Ile Phe Ser Val Thr Ala
100      250      255      260
102 tct gac tcg cta ccg aac aac cac acg gtc acc atg atg gtg caa gtg      992
103 Ser Asp Ser Leu Pro Asn Asn His Thr Val Thr Met Met Val Gln Val
104      265      270      275
106 gag aac gta gag tct cgg ccc cct cgc tgg gtg gag atc ttc tca gtg      1040
107 Glu Asn Val Glu Ser Arg Pro Pro Arg Trp Val Glu Ile Phe Ser Val
108      280      285      290
110 cag cag ttt gac gag aag act aat cag agc ttc tcc ctc cgc gcg ata      1088
111 Gln Gln Phe Asp Glu Lys Thr Asn Gln Ser Phe Ser Leu Arg Ala Ile
112      295      300      305
114 gac ggg gac acg gga atc aat agg gcc atc aac tat acc ctc atc agg      1136
115 Asp Gly Asp Thr Gly Ile Asn Arg Ala Ile Asn Tyr Thr Leu Ile Arg
116 310      315      320      325
118 gat gac gct gac gac ttc ttt tcc ctg gag gtg att gaa gac gga gct      1184
119 Asp Asp Ala Asp Asp Phe Phe Ser Leu Glu Val Ile Glu Asp Gly Ala
120      330      335      340
122 att ctg cac gtg act gag atc gac cgc gac aag ctt gaa aga gag ctt      1232
123 Ile Leu His Val Thr Glu Ile Asp Arg Asp Lys Leu Glu Arg Glu Leu
124      345      350      355
126 ttc aac ctc acc atc gtt gct tac aaa tct act gac gct agc ttt gca      1280
127 Phe Asn Leu Thr Ile Val Ala Tyr Lys Ser Thr Asp Ala Ser Phe Ala
128      360      365      370
130 aca gag gcc cac att ttc atc atc gtc aac gac gtc aat gat cag cga      1328
131 Thr Glu Ala His Ile Phe Ile Ile Val Asn Asp Val Asn Asp Gln Arg

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132	375	380	385	
134	ccc gag ccg ctg cat aaa gaa tac agt att gat atc atg gag gaa act	1376		
135	Pro Glu Pro Leu His Lys Glu Tyr Ser Ile Asp Ile Met Glu Glu Thr			
136	390 395 400 405			
138	cca atg act cta aac ttc aat gaa gaa ttt gga ttc cat gat cga gat	1424		
139	Pro Met Thr Leu Asn Phe Asn Glu Glu Phe Gly Phe His Asp Arg Asp			
140	410 415 420			
142	ttg ggt gaa aac gct caa tac aca gtg gaa ctt gag gac gtg ttc ccg	1472		
143	Leu Gly Glu Asn Ala Gln Tyr Thr Val Glu Leu Glu Asp Val Phe Pro			
144	425 430 435			
146	cca ggg gcg gcg tcc gca ttc tac atc gcg ccg ggg agc ggc tac cag	1520		
147	Pro Gly Ala Ala Ser Ala Phe Tyr Ile Ala Pro Gly Ser Gly Tyr Gln			
148	440 445 450			
150	agg cag acc ttc atc atg ggc acc ata aac cac acc atg ctg gat tac	1568		
151	Arg Gln Thr Phe Ile Met Gly Thr Ile Asn His Thr Met Leu Asp Tyr			
152	455 460 465			
154	gaa gat gtc att ttt cag aac atc atc att aag gtc aaa gca gtg gac	1616		
155	Glu Asp Val Ile Phe Gln Asn Ile Ile Ile Lys Val Lys Ala Val Asp			
156	470 475 480 485			
158	atg aac aac gct agc cac gtg ggc gag gcg ctg gtg tac gtg aac ctg	1664		
159	Met Asn Asn Ala Ser His Val Gly Glu Ala Leu Val Tyr Val Asn Leu			
160	490 495 500			
162	atc aac tgg aac gac gaa ctt ccc atc ttc gag gag agc agc tac tcc	1712		
163	Ile Asn Trp Asn Asp Glu Leu Pro Ile Phe Glu Glu Ser Ser Tyr Ser			
164	505 510 515			
166	gcg tcg ttt aag gag acc gtc ggc gcc ggc ttc ccg gtg gcc acg gtg	1760		
167	Ala Ser Phe Lys Glu Thr Val Gly Ala Gly Phe Pro Val Ala Thr Val			
168	520 525 530			
170	ctc gcc ctc gac aga gac atc gac gac gta gta gtg cat tca ttg atg	1808		
171	Leu Ala Leu Asp Arg Asp Ile Asp Asp Val Val Val His Ser Leu Met			
172	535 540 545			
174	ggc aac gct gtt gac tac ctg ttc ata gat gaa tca acg gga gag atc	1856		
175	Gly Asn Ala Val Asp Tyr Leu Phe Ile Asp Glu Ser Thr Gly Glu Ile			
176	550 555 560 565			
178	ttc gtg agc atg gac gat gcc ttc gac tac cac cga cag aac act cta	1904		
179	Phe Val Ser Met Asp Asp Ala Phe Asp Tyr His Arg Gln Asn Thr Leu			
180	570 575 580			
182	ttt gtt cag gtg cgc gct gac gat act ttg ggc gac ggc cca cac aac	1952		
183	Phe Val Gln Val Arg Ala Asp Asp Thr Leu Gly Asp Gly Pro His Asn			
184	585 590 595			
186	aca gtg acc acc cag ctg gtg ata gaa ctg gag gat gtc aac aac act	2000		
187	Thr Val Thr Thr Gln Leu Val Ile Glu Leu Glu Asp Val Asn Asn Thr			
188	600 605 610			
190	cct ccc acc cta cgc ttg ccc cgt tcg act cca agc gtc gag gag aac	2048		
191	Pro Pro Thr Leu Arg Leu Pro Arg Ser Thr Pro Ser Val Glu Glu Asn			
192	615 620 625			
194	gtt ccc gaa gga tac gag ata tcc cgg gaa atc act gct acc gac ccg	2096		
195	Val Pro Glu Gly Tyr Glu Ile Ser Arg Glu Ile Thr Ala Thr Asp Pro			
196	630 635 640 645			

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198 gac acc agc gcc tac ctg tgg ttc gag atc gac tgg gac tcc acc tgg      2144
199 Asp Thr Ser Ala Tyr Leu Trp Phe Glu Ile Asp Trp Asp Ser Thr Trp
200          650          655          660
202 gcc acc aag cag ggc aga gag acc aac cct act gaa tac gtc ggg tgt      2192
203 Ala Thr Lys Gln Gly Arg Glu Thr Asn Pro Thr Glu Tyr Val Gly Cys
204          665          670          675
206 ata gtt atc gaa acg ata tac ccc acc gag ggc aac cgg ggt tcc gcc      2240
207 Ile Val Ile Glu Thr Ile Tyr Pro Thr Glu Gly Asn Arg Gly Ser Ala
208          680          685          690
210 atc ggg cgc ctc gtg gtg caa gag atc cgg gac aac gtc acc atc gac      2288
211 Ile Gly Arg Leu Val Val Gln Glu Ile Arg Asp Asn Val Thr Ile Asp
212          695          700          705
214 ttc gag gaa ttc gag atg ctt tac ctc acc gtc cgc gtg agg gac ctc      2336
215 Phe Glu Glu Phe Glu Met Leu Tyr Leu Thr Val Arg Val Arg Asp Leu
216 710          715          720          725
218 aac act gtc atc gga gat gac tac gat gag gcg acg ttc acg atc aca      2384
219 Asn Thr Val Ile Gly Asp Asp Tyr Asp Glu Ala Thr Phe Thr Ile Thr
220          730          735          740
222 ata atc gac atg aac gac aac gcg ccg atc ttc gcg aac ggc acg ctg      2432
223 Ile Ile Asp Met Asn Asp Asn Ala Pro Ile Phe Ala Asn Gly Thr Leu
224          745          750          755
226 acg cag acg atg cgc gtg cgc gag ctg gcg gcc agc ggc acg ctc atc      2480
227 Thr Gln Thr Met Arg Val Arg Glu Leu Ala Ala Ser Gly Thr Leu Ile
228          760          765          770
230 ggc tcc gtg ctc gcc acc gac atc gac ggc ccg ctc tac aac caa gtg      2528
231 Gly Ser Val Leu Ala Thr Asp Ile Asp Gly Pro Leu Tyr Asn Gln Val
232          775          780          785
234 cgc tac act ata caa cct aga aac aac act ccc gag gga tta gtg aag      2576
235 Arg Tyr Thr Ile Gln Pro Arg Asn Asn Thr Pro Glu Gly Leu Val Lys
236 790          795          800          805
238 att gac ttc aca act ggt caa att gag gtg gat gcg aac gag gcg atc      2624
239 Ile Asp Phe Thr Thr Gly Gln Ile Glu Val Asp Ala Asn Glu Ala Ile
240          810          815          820
242 gat gca gac gaa ccc tgg cgc ttc tac ttg tac tac acc gtc atc gct      2672
243 Asp Ala Asp Glu Pro Trp Arg Phe Tyr Leu Tyr Tyr Thr Val Ile Ala
244          825          830          835
246 agc gac gag tgc tcc ctg gaa aac cgc acg gaa tgt cct cca gat tcc      2720
247 Ser Asp Glu Cys Ser Leu Glu Asn Arg Thr Glu Cys Pro Pro Asp Ser
248          840          845          850
250 aac tac ttc gaa gtt cca ggc gat atc gaa ata gaa atc atc gac aca      2768
251 Asn Tyr Phe Glu Val Pro Gly Asp Ile Glu Ile Glu Ile Ile Asp Thr
252          855          860          865
254 aac aac aaa gtg cct gag ccg ctc act gag aag ttc aac acg acg gtg      2816
255 Asn Asn Lys Val Pro Glu Pro Leu Thr Glu Lys Phe Asn Thr Thr Val
256 870          875          880          885
258 tac gtc tgg gag aat gcc acg agc ggc gac gag gtg gtc cag ctg tac      2864
259 Tyr Val Trp Glu Asn Ala Thr Ser Gly Asp Glu Val Val Gln Leu Tyr
260          890          895          900
262 tcc cac gac cgt gac aga gac gag ttg tac cac acg gta cga tac acg      2912

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263 Ser His Asp Arg Asp Arg Asp Glu Leu Tyr His Thr Val Arg Tyr Thr
264          905          910          915
266 atg aac ttt gcg gtg aac ccc cga ctg cgg gat ttc ttc gag gtg gac      2960
267 Met Asn Phe Ala Val Asn Pro Arg Leu Arg Asp Phe Phe Glu Val Asp
268          920          925          930
270 ctg gac act ggt cgc ctt gag gtg cat tac ccg ggg gac gaa aaa ttg      3008
271 Leu Asp Thr Gly Arg Leu Glu Val His Tyr Pro Gly Asp Glu Lys Leu
272          935          940          945
274 gac cgc gat ggg gat gag cct aca cat act atc ttt gta aat ttc atc      3056
275 Asp Arg Asp Gly Asp Glu Pro Thr His Thr Ile Phe Val Asn Phe Ile
276 950          955          960          965
278 gat aac ttc ttt tct gat ggt gac ggt agg aga aac cag gac gaa gtt      3104
279 Asp Asn Phe Phe Ser Asp Gly Asp Gly Arg Arg Asn Gln Asp Glu Val
280          970          975          980
282 gaa ata ttt gtc gtt cta ttg gat gtg aac gac aac gct cct gag atg      3152
283 Glu Ile Phe Val Val Leu Leu Asp Val Asn Asp Asn Ala Pro Glu Met
284          985          990          995
286 cca ttg cct gat gaa ctc cgg ttt gat gtt tcc gaa gga gca gtt gct      3200
287 Pro Leu Pro Asp Glu Leu Arg Phe Asp Val Ser Glu Gly Ala Val Ala
288          1000          1005          1010
290 ggt gtc cgt gta ctc cca gaa atc tac gca ccg gac agg gat gaa cca      3248
291 Gly Val Arg Val Leu Pro Glu Ile Tyr Ala Pro Asp Arg Asp Glu Pro
292          1015          1020          1025
294 gac acg gac aac tcg cgt gtc ggt tac gga atc ctg gac ctc acg atc      3296
295 Asp Thr Asp Asn Ser Arg Val Gly Tyr Gly Ile Leu Asp Leu Thr Ile
296 1030          1035          1040          1045
298 acc gac cga gac atc gag gtg ccg gat ctc ttc acc atg atc tcg att      3344
299 Thr Asp Arg Asp Ile Glu Val Pro Asp Leu Phe Thr Met Ile Ser Ile
300          1050          1055          1060
302 gaa aac aaa act ggg gaa ctt gag acc gct atg gac ttg agg ggg tat      3392
303 Glu Asn Lys Thr Gly Glu Leu Glu Thr Ala Met Asp Leu Arg Gly Tyr
304          1065          1070          1075
306 tgg ggc act tac gaa ata ttc att gag gcc ttc gac cac ggc tac ccg      3440
307 Trp Gly Thr Tyr Glu Ile Phe Ile Glu Ala Phe Asp His Gly Tyr Pro
308          1080          1085          1090
310 cag cag agg tcc aac gag acg tac acc ctg gtc atc cgc ccc tac aac      3488
311 Gln Gln Arg Ser Asn Glu Thr Tyr Thr Leu Val Ile Arg Pro Tyr Asn
312          1095          1100          1105
314 ttc cac cac cct gtg ttc gtg ttc ccg caa ccc gac tcc gtc att cgg      3536
315 Phe His His Pro Val Phe Val Phe Pro Gln Pro Asp Ser Val Ile Arg
316 1110          1115          1120          1125
318 ctt tct agg gag cgc gca aca gaa ggc ggc gtt ctg gcg acg gct gcc      3584
319 Leu Ser Arg Glu Arg Ala Thr Glu Gly Gly Val Leu Ala Thr Ala Ala
320          1130          1135          1140
322 aac gag ttc ctg gag ccg atc tac gcc acc gac gag gac ggc ctc cac      3632
323 Asn Glu Phe Leu Glu Pro Ile Tyr Ala Thr Asp Glu Asp Gly Leu His
324          1145          1150          1155
326 gcg ggc agc gtc acg ttc cac gtc cag gga aat gag gag gcc gtt cag      3680
327 Ala Gly Ser Val Thr Phe His Val Gln Gly Asn Glu Glu Ala Val Gln

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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date